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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=9; min=43; sec=57; ms=320;]

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Reviewer Comments:

<210> 57

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is glycine or alanine.

<220>

<221> misc_feature

<222> (7)..(7)

<223> n is threonine or cysteine.

<220>

<221> misc_feature

<222> (8)..(8)

<223> n is threonine or cysteine.

<400> 57

nggaganntg

10

The above <220>-<223> sections describing the "n's" are errored: "n" can only represent a single nucleotide; it cannot represent an amino

acid.

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X can be a or g.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X can be t or c.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X can be a or g.

<400> 130

Xaa Gly Gly Ala Gly Ala Xaa Thr Thr Xaa
1 5 10

If the above <220>-<223> sections regarding the "Xaa's" are defining them as nucleotides, they are erroneous. If they are denoting amino acids, please spell them out in the <223> responses.

Application No: 10574333

Version No: 1.0

Input Set:

Output Set:

Started: 2010-07-21 14:54:12.726

Finished: 2010-07-21 14:54:16.948

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms

Total Warnings: 100

Total Errors: 0

No. of SeqIDs Defined: 134

Actual SeqID Count: 134

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W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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W 213	Artificial or Unknown found in <213> in SEQ ID (39)
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Input Set:

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Total Warnings: 100

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No. of SeqIDs Defined: 134

Actual SeqID Count: 134

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> The Regents of the University of California
Karin, Michael
Bonizzi, Giuseppina
Bebien, Mahali

<120> Compositions and Methods for Gene Expression

<130> UCSD-10835

<140> 10574333

<141> 2010-07-21

<150> US 60/508349

<151> 2003-10-01

<150> PCT/US2004/032246

<151> 2004-09-29

<160> 134

<170> PatentIn version 3.5

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<211> 700

<212> DNA

<213> Mus musculus

<400> 1

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gccctacgtt agaattgcac ttcccgggaa tgactgtagt gagactttgg ctgggaatcc	180
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tgtgcctttg acagcccctt agtttctcta tctgcaggat gggagcatta agctctacga	420
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aaggtctcag caccacggg agccggggac actgagggcg ccaagaaggg ggtgggtagg	540
tagggaactg gaaggcgccg tgcctccgag gggatgcggc tcagagaccc cagccacact	600
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<210> 2

<211> 10
<212> DNA
<213> Mus musculus

<400> 2
gggagacctg

10

<210> 3
<211> 933
<212> PRT
<213> Homo sapiens

<400> 3

Met Glu Ser Cys Tyr Asn Pro Gly Leu Asp Gly Ile Ile Glu Tyr Asp
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Asp Phe Lys Leu Asn Ser Ser Ile Val Glu Pro Lys Glu Pro Ala Pro
20 25 30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
50 55 60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
85 90 95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Gln Cys Ser Glu Leu Gly Ile Cys Ala Val Ser Val Gly Pro Lys Asp
115 120 125

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Gly Thr Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
165 170 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
195 200 205

Leu Lys Pro Val Thr Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
340 345 350

Gly Ser His Met Gly Gly Gly Ser Gly Gly Ala Ala Gly Gly Tyr Gly
355 360 365

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Pro Ser Ser Leu Ala
370 375 380

Tyr Ser Pro Tyr Gln Ser Gly Ala Gly Pro Met Arg Cys Tyr Pro Gly
385 390 395 400

Gly Gly Gly Gly Ala Gln Met Ala Ala Thr Val Pro Ser Arg Asp Ser			
405	410	415	
Gly Glu Glu Ala Ala Glu Pro Ser Ala Pro Ser Arg Thr Pro Gln Cys			
420	425	430	
Glu Pro Gln Ala Pro Glu Met Leu Gln Arg Ala Arg Glu Tyr Asn Ala			
435	440	445	
Arg Leu Phe Gly Leu Ala His Ala Ala Pro Ser Pro Thr Arg Leu Leu			
450	455	460	
Arg His Arg Gly Arg Arg Ala Leu Leu Ala Gly Gln Arg His Leu Leu			
465	470	475	480
Thr Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu Ala Ile Ile			
485	490	495	
His Gly Gln Thr Ser Val Ile Glu Gln Ile Val Tyr Val Ile His His			
500	505	510	
Ala Gln Asp Leu Gly Val Val Asn Leu Thr Asn His Leu His Gln Thr			
515	520	525	
Pro Leu His Leu Ala Val Ile Thr Gly Gln Thr Ser Val Val Ser Phe			
530	535	540	
Leu Leu Arg Val Gly Ala Asp Pro Ala Leu Leu Asp Arg His Gly Asp			
545	550	555	560
Ser Ala Met His Leu Ala Leu Arg Ala Gly Ala Gly Ala Pro Glu Leu			
565	570	575	
Leu Arg Ala Leu Leu Gln Ser Gly Ala Pro Ala Val Pro Gln Leu Leu			
580	585	590	
His Met Pro Asp Phe Glu Gly Leu Tyr Pro Val His Leu Ala Val Arg			
595	600	605	
Ala Arg Ser Pro Glu Cys Leu Asp Leu Leu Val Asp Ser Gly Ala Glu			
610	615	620	

Val Glu Ala Thr Glu Arg Gln Gly Gly Arg Thr Ala Leu His Leu Ala
625 630 635 640

Thr Glu Met Glu Glu Leu Gly Leu Val Thr His Leu Val Thr Lys Leu
645 650 655

Arg Ala Asn Val Asn Ala Arg Thr Phe Ala Gly Asn Thr Pro Leu His
660 665 670

Leu Ala Ala Gly Leu Gly Tyr Pro Thr Leu Thr Arg Leu Leu Leu Lys
675 680 685

Ala Gly Ala Asp Ile His Ala Glu Asn Glu Glu Pro Leu Cys Pro Leu
690 695 700

Pro Ser Pro Pro Thr Ser Asp Ser Asp Ser Asp Ser Glu Gly Pro Glu
705 710 715 720

Lys Asp Thr Arg Ser Ser Phe Arg Gly His Thr Pro Leu Asp Leu Thr
725 730 735

Cys Ser Thr Leu Val Lys Thr Leu Leu Leu Asn Ala Ala Gln Asn Thr
740 745 750

Met Glu Pro Pro Leu Thr Pro Pro Ser Pro Ala Gly Pro Gly Leu Ser
755 760 765

Leu Gly Asp Thr Ala Leu Gln Asn Leu Glu Gln Leu Leu Asp Gly Pro
770 775 780

Glu Ala Gln Gly Ser Trp Ala Glu Leu Ala Glu Arg Leu Gly Leu Arg
785 790 795 800

Ser Leu Val Asp Thr Tyr Arg Gln Thr Thr Ser Pro Ser Gly Ser Leu
805 810 815

Leu Arg Ser Tyr Glu Leu Ala Gly Gly Asp Leu Ala Gly Leu Leu Glu
820 825 830

Ala Leu Ser Asp Met Gly Leu Glu Glu Gly Val Arg Leu Leu Arg Gly
835 840 845

Pro Glu Thr Arg Asp Lys Leu Pro Ser Thr Glu Val Lys Glu Asp Ser

Ala Tyr Gly Ser Gln Ser Val Glu Gln Glu Ala Glu Lys Leu Gly Pro
 865 870 875 880

Pro Pro Glu Pro Pro Gly Gly Leu Ser His Gly His Pro Gln Pro Gln
 885 890 895

Val Thr Asp Leu Leu Pro Ala Pro Ser Pro Leu Pro Gly Pro Pro Val
 900 905 910

Gln Arg Pro His Leu Phe Gln Ile Leu Phe Asn Thr Pro His Pro Pro
 915 920 925

Leu Ser Trp Asp Lys
 930

<210> 4

<211> 3001

<212> DNA

<213> Homo sapiens

<400> 4

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cctggccgga gccactagac agagccgggc ctagcccaga gacatggaga gttgctacaa 180

cccaggctctg gatggtatta ttgaatatga tgatttcaaa ttgaactcct ccattgtgga 240

acccaaggag ccagccccag aaacagctga tggcccctac ctgggtgatcg tggacagcc 300

taagcagaga ggcttccgat ttgatattgg ctgtgaaggc ccctcccatg gaggactgcc 360

cgggtgctcc agtgagaagg gccgaaagac ctatcccact gtcaagatct gtaactacga 420

gggaccagcc aagatcgagg tggacctggt aacacacagt gacccacctc gtgctcatgc 480

ccacagtctg gggggcaagc aatgctcgga gctggggata tgcgccgttt ctgtggggcc 540

caaggacatg actgcccaat ttaacaacct ggggtgctct catgtgacta agaagaacat 600

gatggggact atgatacaaa aacttcagag gcagcggctc gcctctaggc ccaggggcct 660

tacggaggcc gagcagcggg agctggagca agaggccaaa gaactgaaga aggtgatgga 720

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t						3060

Met Asp Asn Cys Tyr Asp Pro Gly Leu Asp Gly Ile Pro Glu Tyr Asp
1 5 10 15

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Glu Ile Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Lys Pro Gln Gly Leu Thr Glu Ala Glu Arg Arg Glu Leu Glu Gln
165 170 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
195 200 205

Leu Lys Pro Val Ile Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
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Gly Ser His Met Gly Gly Gly Ser Gly Gly Ser Ala Gly Gly Tyr Gly

Gly Ala Gly Gly Gly Gly Ser Leu Gly Phe Phe Ser Ser Ser Leu Ala
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Tyr Asn Pro Tyr Gln Ser Gly Ala Ala Pro Met Gly Cys Tyr Pro Gly
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 405 410 415

Gly Glu Gly Ala Glu Glu Pro Arg Thr Pro Pro Glu Ala Pro Gln Gly
 420 425 430

Glu Pro Gln Ala Leu Asp Thr Leu Gln Arg Ala Arg Glu Tyr Asn Ala
 435 440 445

Arg Leu Phe Gly Leu Ala Gln Arg Ser Ala Arg Ala Leu Leu Asp Tyr
 450 455 460

Gly Val Thr Ala Asp Ala Arg Ala Leu Leu Ala Gly Gln Arg His Leu
 465 470 475 480

Leu Met Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu